

2590
1705

#15



ENTERED

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,304B

DATE: 11/13/2002

TIME: 14:04:16

Input Set : A:\09993304.txt

Output Set: N:\CRF4\11132002\I993304B.raw

3 <110> APPLICANT: Jackowski, George
 5 <120> TITLE OF INVENTION: IG Heavy Chain IG Kappa and IG Lambda Biopolymer Markers
 Predictive of AD
 7 <130> FILE REFERENCE: 2132.095
 9 <140> CURRENT APPLICATION NUMBER: US 09/993,304B
 10 <141> CURRENT FILING DATE: 2001-11-23
 12 <160> NUMBER OF SEQ ID NOS: 7
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 18
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: MISC_FEATURE
 23 <222> LOCATION: (1)..(1)
 24 <223> OTHER INFORMATION: X may be Q or K.
 27 <400> SEQUENCE: 1
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 30 1 5 10 15
 33 Arg Val
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 17
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 2
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 48 Ser
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 18
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Homo sapiens
 57 <400> SEQUENCE: 3
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 63 Arg Glu
 67 <210> SEQ ID NO: 4
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 69 <212> TYPE: PRT
 70 <213> ORGANISM: Homo sapiens
 72 <400> SEQUENCE: 4
 74 Lys Gly Leu Glu Trp Val Ala Gly Leu Ser Trp Asn Ser Asp Asn Ile
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 78 Arg Tyr

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83 <211> LENGTH: 21
84 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
87 <400> SEQUENCE: 5
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93 Phe Ser Gln Lys Ser
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99 <212> TYPE: PRT
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111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 7
115 Arg Ala Gly Tyr Arg Ile Asp Ser Trp Gly Gln Gly Thr Leu Val Thr
116 1 5 10 15

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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Input Set : A:\09993304.txt

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L:29 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0